

Amendments to the Claim:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1-17 (cancelled)

18 (withdrawn - currently amended). A method of improving the shelf life and/or the quality of an edible product comprising adding to the product ~~a lactic acid bacterial strain~~ the starter culture composition according to claim 25 that is defective in its pyruvate metabolism.

19 (withdrawn). A method according to claim 18 wherein the lactic acid bacterial strain essentially does not produce lactic acid.

20 (withdrawn). A method according to claim 18 wherein the lactic acid bacterial strain is defective in its ability to express at least one enzyme selected from the group consisting of pyruvate formate lyase, pyruvate dehydrogenase, lactate dehydrogenase, acetolactate synthetase, second acetolactate synthetase, acetolactate decarboxylase and diacetyl reductase.

21 (withdrawn). A method according to claim 18 wherein the edible product is selected from the group consisting of milk, flour dough, meat, wine and a plant material.

22 (withdrawn). A method according to claim 21 wherein the edible product is non-pasteurized milk.

23 (withdrawn). A method according to claim 18 wherein the lactic acid bacterial strain is added to the product at its site of production.

24 (withdrawn). A method according to claim 23 wherein the lactic acid bacterial strain is added to raw milk following milking.

25 (original). A starter culture composition comprising a lactic acid bacterium and a lactic acid bacterial helper organism that is defective in its pyruvate metabolism, said helper organism being capable of enhancing the growth rate and/or

controlling the metabolic activity of the lactic acid bacterium.

26 (original). A composition according to claim 25 wherein the helper organism essentially does not produce lactic acid.

27 (original). A composition according to claim 25 wherein the helper organism is defective in its ability to produce at least one enzyme selected from the group consisting of pyruvate formate lyase, pyruvate dehydrogenase, lactate dehydrogenase, acetolactate synthetase, second acetolactate synthetase, acetolactate decarboxylase and diacetyl reductase.

28 (original). A composition according to claim 25 wherein the helper organism is *Lactococcus lactis* subs. *lactis* strain DN223 deposited under the accession No. DSM 11036.

29 (original). A composition according to claim 25 wherein the helper organism is *Lactococcus lactis* subs. *lactis* strain DN224 deposited under the accession No. DSM 11037.

30 (original). A composition according to claim 25 wherein a gene coding for an enzyme that is capable of regenerating NAD^+ is overexpressed in the helper organism.

31 (original). A composition according to claim 30 wherein the enzyme catalyses the reduction of O_2 to H_2O or H_2O_2 .

32 (original). A composition according to claim 31 wherein the enzyme is $\text{NADH}:\text{H}_2\text{O}$ oxidase including the enzyme having the sequence SEQ ID NO:2.

33 (original). A composition according to claim 30 wherein the helper organism is an Ldh- strain.

34 (original). A composition according to claim 25 that comprises two or more different lactic acid bacterial strains.

35 (withdrawn). An isolated or non-naturally occurring lactic acid bacterium that is defective in its ability to express lactic acid dehydrogenase and in which a gene encoding a protein capable of regenerating NAD^+ is overexpressed, wherein the gene capable of regenerating NAD^+ that is overexpressed codes for an enzyme catalysing the reduction of O_2 to H_2O or H_2O_2 .

36 (withdrawn). A bacterium according to claim 35 which is defective in its ability to express at least one further enzyme

selected from the group consisting of pyruvate formate lyase, pyruvate dehydrogenase, acetolactate synthetase, second acetolactate synthetase, acetolactate decarboxylase and diacetyl reductase.

37 (withdrawn - currently amended). A bacterium according to claim ~~37~~ 35 wherein the gene capable of regenerating NAD^+ that is overexpressed codes for an enzyme catalyzing the reduction of O_2 to H_2O or H_2O_2 .

38 (withdrawn). A bacterium according to claim 35 wherein the enzyme is $\text{NADH:H}_2\text{O}$ oxidase including the enzyme having the sequence SEQ ID NO:2.

39 (withdrawn). An isolated DNA fragment derived from a lactic acid bacterium comprising a gene coding for a polypeptide having $\text{NADH:H}_2\text{O}$ oxidase activity.

40 (withdrawn). A DNA fragment according to claim 39 which is selected from the group consisting of the sequence shown in SEQ NO ID:1 and a variant or derivative hereof which is at least 50% identical with said sequence.

41 (withdrawn). A recombinant DNA molecule comprising the DNA fragment of claim 39.

42 (withdrawn). A recombinant DNA molecule comprising the DNA fragment of claim 40.

43 (withdrawn). The bacterium of claim 35 which is selected from the group consisting of bacteria of the genera *Lactococcus*, *Lactobacillus*, *Streptococcus*, *Leuconostoc*, *Pediococcus*, *Propionibacterium*, and *Bifidobacterium*.

44 (withdrawn). The bacterium of claim 35 which is a strain of *Lactococcus lactis*, *Lactobacillus bulgaricus*, *Streptococcus thermophilus*, or *Lactobacillus delbruecki*, *Leuconostoc mesenteroides*.

45 (withdrawn). The bacterium of claim 35 which is a strain of *Lactococcus lactis*.

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REMARKS

1. Claim 18 has been amended so as to be dependent on claim 25, and thereby rejoinable under MPEP 821.04.

2. Claim 37 has been amended because it was dependent on itself.

Respectfully submitted,

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